



1 50
 EG327 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVATAVLA TLLFATVQAS.
 BZ198 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
 BZ10 MNKISRRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
 H15 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
 EG329 MNEILRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 PMC21 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 H38 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 P20 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLSATVQAN
 Z2491 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 Consensus MN-I-RIIWN SALNAWV-VS ELTRNHTKRA SATV-TAVLA TLL-ATVQA-

C1

51 100
 EG327 TTDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
 BZ198 ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
 BZ10 ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
 H15 ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
 EG329 ANNEEQEEDL YLDPVLRRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
 PMC21 ANNEEQEEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
 H38 ATDED..EEE ELEPVVRSAL VLQFMIDKEG NGENE.STGN IGWSIYYDNH
 P20 ATDTD..EDE ELESVARSA VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
 Z2491 ATDED..EEE ELESVQR.SV VGSIQASMEG SGELET...I SLSMTNDSKE
 H41 ATDED..EEE ELESVQR.SV VGSIQASMEG SVELET...I SLSMTNDSKE
 Consensus ----- L--V-R-- V-----EG --E-E-----

V1

101 150
 EG327 GVLTAGTITL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTDLTSVG
 BZ198 RVLKAGAITL KAGDNLKIKQ NTNENTNDSSFTYSLK KDLTDLTSVE
 BZ10 RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
 H15 RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
 EG329 GVLTAREITL KAGDNLKIKQ NG...TN...FTYSLK KDLTDLTSVG
 PMC21 GVLTAREITL KAGDNLKIKQ NG...TN...FTYSLK KDLTDLTSVG
 H38 NTLHGATVTL KAGDNLKIKQ NTNKNENT NDSSFTYSLK KDLTDLTSVE
 P20 TLHG.ATVTL KAGDNLKIKQ SGKD.....FTYSLK KELKDLTSVE
 Z2491 FVDPYIVVTL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTGLINVE
 H41 FVDPYIVVTL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTGLINVE
 Consensus ----- TL KAGDNLKIKO ----- ----- FTYSLK K-L--L--V-
 V1 C2 V2 C3

FIG. 1

	151	200
EG327	TEKLSFSANS NKVNITSDTK GLNFAKKTAE TNGDTTVHLN GIGSTLTDTL	
BZ198	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL	
BZ10	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL	
H15	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL	
EG329	TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL	
PMC21	TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL	
H38	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL	
P20	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL	
Z2491	TEKLSFGANG KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL	
H41	TEKLSFGANG KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML	
Consensus	<u>TEKLSF-AN- -KVNI-SDTK GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L</u>	

C3

	201	250
EG327	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
BZ198	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
BZ10	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
H15	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
EG329	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
PMC21	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
H38	LNTGATTNVT NDNVTDDKKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
P20	AGSSASHVDA GNQST.. HYT RAASIKDVLN AGWNIKGVKT GSTTGQSENV	
Z2491	AGSSASHVDA GNQST.. HYT RAASIKDVLN AGWNIKGVKT GSTTGQSENV	
H41	LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVP GTTAS.. DNV	
Consensus	<u>-----A-----T----- RAAS-KDVLN AGWNIKGVK- G-T-----NV</u>	

V3

C4

V4

	251	300
EG327	DFVRTYDTVE FLSADTKTTT VNVESKDNGK RTEVKIGAKT SVIKEKDGL	
BZ198	DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT SVIKEKDGL	
BZ10	DFVRTYDTVE FLSADTKTTT VNVESKDNGK RTEVKIGAKT SVIKEKDGL	
H15	DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT SVIKEKDGL	
EG329	DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT SVIKEKDGL	
PMC21	DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT SVIKEKDGL	
H38	DFVHTYDTVE FLSADTKTTT VNVESKDNGK RTEVKIGAKT SVIKEKDGL	
P20	DFVRTYDTVE FLSADTKTTT VNVESKDNGK RTEVKIGAKT SVIKEKDGL	
Z2491	DFVRTYDTVE FLSADTKTTT VNVESKDNGK RTEVKIGAKT SVIKEKDGL	
H41	DFVRTYDTVE FLSADTKTTT VNVESKDNGK KTEVKIGAKT SVIKEKDGL	
Consensus	<u>DFV-TYDTVE FLSADTKTTT VNVESKDNGK -TEVKIGAKT SVIKEKDGL</u>	

C5

	301	350
EG327	VTGKDKGEND SSTDKGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
BZ198	VTGKGKDENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
BZ10	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H15	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
EG329	VTGKDKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
PMC21	VTGKDKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H38	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
P20	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
Z2491	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H41	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
Consensus	<u>VTGK-K-EN- SSTD-GEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK</u>	

C5

	351	400
EG327	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVMYDGVNGD ALNVNQLQNS	
BZ198	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
BZ10	FETVTSGTKV TFASGNGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
H15	FETVTSGTKV TFASGNGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
EG329	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVMYDGVNGD ALNVNQLQNS	
PMC21	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVMYDGVNGD ALNVNQLQNS	
H38	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
P20	FETVTSGTKV TFASGNGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
Z2491	FETVTSGTNV TFASGKGTTA TVSKDDQGNI TVMYDGVNGD ALNVNQLQNS	
H41	FETVTSGTKV TFASGNGTTA TVSKDDQGNI TVKYDGVNGD ALNVNQLQNS	
Consensus	<u>FETVTSGT-V TFASG-GTTA TVSKDDQGNI TV-YDGVNGD ALNVNQLQNS</u>	

C5

	401	450
EG327	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
BZ198	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
BZ10	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
H15	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
EG329	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
PMC21	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
H38	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
P20	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
Z2491	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EISRNCKNID	
H41	GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID	
Consensus	<u>GWNLDKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>	

C5

		451		500	
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

		501		550	
EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

		551		600	
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

FIG. 1

	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

FIG. 1

1 70

H15 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 BZ10 ATGAACAAAA TATCCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 BZ198 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 P20 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT AGTCGTATCC GAGCTCACAC
 H38 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 Z2491 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 H41 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 EG329 ATGAACGAAA TATTGCGAT CATTGGAAT AGGCCCTCA ATGCCTGGGT CGTTGTATCC GAGCTCACAC
 PMC21 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT CGTCGTATCC GAGCTCACAC
 EG327 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 Consensus ATGAAC-AAA TAT--CGCAT CATTGGAAT AG-GCCCTCA ATGC-TGGGT -G--GTATCC GAGCTCACAC

C1

71 140

H15 GCAACCACAC CAAACCGGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 BZ10 GCAACCACAC CAAACCGGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 BZ198 GCAACCACAC CAAACCGGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 P20 GCAACCACAC CAAACCGGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGCTGT CCGCAACGGT
 H38 GCAACCACAC CAAACCGGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACGCTGTTGT TTGCAACGGT
 Z2491 GCAACCACAC CAAACCGGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 H41 GCAACCACAC CAAACCGGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 EG329 GCAACCACAC CAAACCGGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 PMC21 GCAACCACAC CAAACCGGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 EG327 GCAACCACAC CAAACCGGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 Consensus GCAACCACAC CAAACCGGCC TCCGCAACCG TG--GACCGC CGTATTGGCG AC-CTG-TGT --GCAACGGT

C1

141 210

H15 TCAGGCGAAT GCTACCGATG ACGAC..... .GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 BZ10 TCAGGCGAAT GCTACCGATG ACGAC..... .GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 BZ198 TCAGGCGAAT GCTACCGATG ACGAC..... .GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 P20 TCAGGCGAAT GCTACCGATA CCGAT..... .GAAGATGAA GAGTTAGAAT CCGTAGCACG CTCTGCTCTG
 H38 TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAC CCGTAGTACG CTCTGCTCTG
 Z2491 TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTGTCGTA
 H41 TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTG...TC
 EG329 TCAGGCGAAGT GCTAACATG AAGAGCAAGA AGAAGATTAA TATTTAGACC CCGTGCTACG CACTGTTGCC
 PMC21 TCAGGCGAAGT GCTAACATG AAGAGCAAGA AGAAGATTAA TATTTAGACC CCGTACAACG CACTGTTGCC
 EG327 TCAGGCGAGT ACTACCGATG ACGAC..... .GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 Consensus TCAGGC-A-T -CTA-C-AT- --GA----- --GA---A -A-TTAGA-- CCGT---ACG C-CTG-----

C1

V1

	211		280					
H15	GTGTTGAGCT	TCGGTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...	T	TCAAATTGGG
BZ10	GTGTTGAGCT	TCGGTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...	T	TCAAATTGGG
BZ198	GTGTTGAGCT	TCGGTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...	T	TCAAATTGGG
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...	T	ATAGGTTGGA
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...	T	ATAGGTTGGA
Z2491	GGG...AGCAT	TCAAG.CCAG	TATGGAAGGC	ACGGGCGAAT	TGAAACGAT	ATCAT...	T	ATCAATGACT
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	ACGGTCGAAT	TGAAACGAT	A.....		TCATTATCAA
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAGT	AGAAGAAAAT		TCAGATTGGG
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAGT	AGAAGAAAAT		TCAGATTGGG
EG327	GTGTTGAGCT	TCGGTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTAC	AGAAGA...	T	TCAAATTGGG
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----		

V1

	281		350				
H15	CAGTATATT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
BZ10	CAGTATATT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
BZ198	CAGTATATT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCCTC	AAAGCCGGCG	ACAACCTGAA
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCCTC	AAAGCCGGCG	ACAACCTGAA
Z2491	AACGACAGCA	AGGAATTGT	AGACCCATAC	ATAGTA...	.GTTACCCCTC	AAAGCCGGCG	ACAACCTGAA
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCCTC	AAAGCCGGCG	ACAACCTGAA
EG329	CAGTATATT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
PMC21	CAGTATATT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
EG327	GAGTATATT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCTC	AAAGCCGGCG	ACAACCTGAA
Consensus	-----A-----	-----	-----	-----	--T-ACCCCTC	AAAGCCGGCG	ACAACCTGAA

V1

C2

	351		420				
H15	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ10	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ198	AATCAAACAA	AACACCAATG	AAAACACC..	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
P20	AATCAAACAA	AGCGGCAAAG	A.....	CTTCACCTA	CTCGCTGAAA
H38	AATCAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA
Z2491	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
H41	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
EG329	AATCAAACAA	AAC..	G..GCACAA	ACTTCACCTA	CTCGCTGAAA
PMC21	AATCAAACAA	AAC..	G..GCACAA	ACTTCACCTA	CTCGCTGAAA
EG327	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
Consensus	AATCAAACAA	A-C-----	-----	-----	-----	CTTCACCTA	CTC-CTGAAA

C2

V2

C3

421 490

H15 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 BZ10 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 BZ198 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 P20 AAAGAGCTGA AAGACCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 H38 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AATAAAGTCA
 Z2491 AAAGACCTCA CAGGCCTGAT CAATGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AAGAAAGTCA
 H41 AAAGACCTCA CAGGCCTGAT CAATGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AAGAAAGTCA
 EG329 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACGGC AATAAAGTCA
 PMC21 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACGGC AATAAAGTCA
 EG327 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACAGC AATAAAGTCA
 Consensus AAAGA-CT-A -AG--CTGA- CA-TGTG-A ACTGAAAAAT TATCGTT-G CGCAAAC-G- AA-AAAGTCA

C3

491 560

H15 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 BZ10 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 BZ198 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 P20 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 H38 ACATCACAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 Z2491 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 H41 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 EG329 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 PMC21 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 EG327 ACATCACAAG CGACACCAAA GGCTTGAATT TCGCGAAAAA AACGGCTGAG ACCAACGGCG ACACCACGGT
 Consensus ACATCA-AAG CGACACCAAA GGCTTGAATT T-GCGAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT

C3

561 630

H15 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 BZ10 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 BZ198 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 P20 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
 H38 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 Z2491 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
 H41 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATATGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 EG329 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 PMC21 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 EG327 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAAC AAACGTAACC
 Consensus TCATCTGAAC GGTAT-GGTT CGACTTTGAC CGATA-GCT- --G--T-C-- --GC--C-- --G--C-

C3

V3

	631				
H15	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				700
BZ10	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				
BZ198	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				
P20	GGTAACCAAA GTACACATTA C.....ACT CGTGCAGCAA GTATTAAAGA TGTGTTGAAT GCAGGCTGGA				
H38	AACGACAACG TTACCGATGA CAAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				
Z2491	GGTAACCAAA GTACACATTA C.....ACT CGTGCAGCAA GTATTAAAGA TGTGTTGAAT GCAGGCTGGA				
H41	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				
EG329	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA				
PMC21	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA				
EG327	AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCAGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA				
Consensus	<u>----AC-A--</u> <u>-TAC--AT-A</u> <u>C-----A--</u> CGTGC-GCAA G--TTAA-GA -GT-TT-AA- GC-GG-TGGA				
	V3			C4	
	701				770
H15	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
BZ10	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTC GATTCGTCC GCACTTACGA				
BZ198	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
P20	ATATTAAGGG TGTTAAACT GGCTAACCAA CTGGTCATC AGAAAATGTC GATTCGTCC GCACTTACGA				
H38	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC ACACCTTACGA				
Z2491	ATATTAAGGG TGTTAAACT GGCTAACCAA CTGGTCATC AGAAAATGTC GATTCGTCC GCACTTACGA				
H41	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
EG329	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
PMC21	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
EG327	ACATTAAGG CGTTAACCCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA				
Consensus	<u>A-ATTA-GG</u> <u>-GTTAA-C-</u> <u>GG--CAACA-</u> <u>CT-----TC</u> <u>-GA-AA-GT-</u> GATTCGTCC -CACTTACGA				
	C4	V4		C5	
	771				840
H15	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
BZ10	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
BZ198	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
P20	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
H38	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
Z2491	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
H41	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
EG329	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
PMC21	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
EG327	CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAACGACT GTTAATGTGG AAACCAAAGA CAACGGCAAG				
Consensus	<u>CACAGTCGAG</u> <u>TTCTTGAGCG</u> <u>CAGATACGAA</u> <u>ACAACGACT</u> GTTAATGTGG AAACCAAAGA CAACGGCAAG				
			C5		
	841				910
H15	AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
BZ10	AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
BZ198	AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
P20	AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
H38	AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
Z2491	AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
H41	AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
EG329	AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
PMC21	AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
EG327	AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
Consensus	<u>A-AAACCGAAG</u> <u>TTAAAATCGG</u> <u>TCGGAAGACT</u> TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA				
			C5		

911 980

H15 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 BZ10 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 BZ198 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 P20 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 H38 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 Z2491 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 H41 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 EG329 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 PMC21 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 EG327 AAGACAAAGG CGAGAATGAT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
 Consensus AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA

C5

981 1050

H15 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 BZ10 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 BZ198 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 P20 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 H38 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 Z2491 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 H41 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 EG329 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 PMC21 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 EG327 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
 Consensus TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG

C5

1051 1120

H15 TTTGAAACCG TTACATCAGG CACAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 BZ10 TTTGAAACCG TTACATCAGG CACAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 BZ198 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 P20 TTTGAAACCG TTACATCAGG CACAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 H38 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 Z2491 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 H41 TTTGAAACCG TTACATCAGG CACAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 EG329 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 PMC21 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 EG327 TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA
 Consensus TTTGAAACCG TTACATCAGG CACAAA-GTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA

C5

1121 1190

H15 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 BZ10 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 BZ198 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 P20 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 H38 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 Z2491 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 H41 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 EG329 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 PMC21 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 EG327 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT
 Consensus AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTTAAA TGCGGGCAT GCCCTAAACG TCAATCAGCT

C5

	1191		1260				
H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ10	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACGGGTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT

C5

	1261		1330				
H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ10	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTAGCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTA-CC

C5

	1331		1400				
H15	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
BZ10	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
BZ198	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
P20	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
H38	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
Z2491	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
H41	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
EG329	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
PMC21	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
EG327	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTCG	TCGGCGCGGG
Consensus	GCAACGG- <u>AA</u>	AAATATCGAC	ATGCCACTT	CGATG-C-CC	GCA- <u>TTT</u>	AGCGTTTCG	TCGG-G-GCGG

C5

	1401		1470					
H15	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ10	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ198	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TACCAACAAA
P20	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H38	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Z2491	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H41	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
EG329	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	GGGGGACGCA	TTGAATGTCG	GCAGCAAGGA	GGACAACAAA
PMC21	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	GGGGGACGCA	TTGAATGTCG	GCAGCAAGGA	GGACAACAAA
EG327	GCCGGATGCG	CCCAC	TTAA	GGCTGGATGA	GGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Consensus	GCC-GATGCG	CCCAC	TTAA	GGCTGGAT--	--GG-CGC-	TTGAATGTCG	GCAGCAAG-A	--CAACAAA

C5

1471 1540

H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
BZ10	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
BZ198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTAAAGAGG</u>	<u>GGGATGTTAC</u>	<u>AAACGTCGCA</u>	<u>CAACTTAAAG</u>

C5

1541 1610

H15	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCCAAGC
BZ10	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCCAAGC
BZ198	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
P20	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGAA	CGGCAACGCG	CGCGCGGGTA	TCGCCCCAAGC
H38	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
Z2491	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
H41	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGAA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
EG329	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
PMC21	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
EG327	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CCTGCGGGCA	TCGCCCCAAGC
Consensus	<u>GTGTGGCGCA</u>	<u>AAACTTGAAC</u>	<u>AACCGCATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGCG</u>	<u>CG-GCGG-A</u>	<u>TCGCCCCAAGC</u>

C5

1611 1680

H15	GATTGCAACC	GCAGGGTTGG	CTCAGGCCGA	TTTGCCTCGG	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
BZ10	GATTGCAACC	GCAGGGTTGG	CTCAGGCCGA	TTTGCCTCGG	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
BZ198	GATTGCAACC	GCAGGGTCTAG	TTCAGGCCGA	TCTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGACACT
P20	GATTGCAACC	GCAGGGTCTGG	CTCAGGCCGA	TTTGCCTCGG	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
H38	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TCTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
Z2491	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TCTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
H41	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TCTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
EG329	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TTTGCCTCGG	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
PMC21	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TTTGCCTCGG	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
EG327	GATTGCAACC	GCAGGGTCTGG	TTCAGGCCGA	TCTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGCACT
Consensus	<u>GATTGCAACC</u>	<u>GCAGGG-T-G</u>	<u>-TCAGGC-TA</u>	<u>T-TGCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGGCG--ACT</u>

C5

	1681	1750
H15	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG	
BZ10	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG	
BZ198	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCAAGTA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
P20	TATCTCGGG AAGCGGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG	
H38	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
Z2491	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCCAGTA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
H41	TATCTCGGG AAGCGGGTTA CGCCATCGGC TACTCAAGCA TTTCTGCGGG CGGAAATTGG ATTATCAAGG	
EG329	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCCAGTA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
PMC21	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCCAGTA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
EG327	TATCGCGGG AAGCGGGTTA CGCCATCGGC TACTCAAGCA TTTCTGACAC CGGAAATTGG ATTATCAAGG	
Consensus	TATCGCGGG AAGCGGGTTA -GCCATCGGC TACTC-AG-A TTTC-G-C-- -GG-AATTGG -TTATCAA-G	
		C5
	1751	1815
H15	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
BZ10	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTACTTC CGCATCTTC CGT TT TATCAGT GTTAA	
BZ198	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAAT GTTAA	
P20	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTACTTC CGCATCTTC CGT TT TATCAGT GTTAA	
H38	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
Z2491	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
H41	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
EG329	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
PMC21	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
EG327	GCA CG GGCTTC CGGC AA ATT CG CGGGGGCATT TCGGTGCTTC CGCATCTTC CGT TT TATCAGT GTTAA	
Consensus	GCA CG GGCTTC CGGC AA ATT CG CGGGGG-CATT TCGGT-CTTC CGCATCTTC CGT TT TATCA-T GTTAA	
		C5

FIG. 2

	401		450
H41	<u>SKAVAGSSGK</u> VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
PMC21	<u>SKAVAGSSGK</u> VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
H41Studel	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
PMC21Bglde1	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
PMC21C1C5	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
	C5		
	451		500
H41	<u>TPQFSSVSLG</u> AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD		
PMC21	<u>TPQFSSVSLG</u> AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD		
H41Studel	TPQFSSVSLG AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD		
PMC21Bglde1	TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD		
PMC21C1C5	TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD		
	C5		
	501		550
H41	<u>VTNVAQLKGV</u> AONLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA		
PMC21	<u>VTNVAQLKGV</u> AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA		
H41Studel	VTNVAQLKGV AONLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA		
PMC21Bglde1	VTNVAQLKGV AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA		
PMC21C1C5	VTNVAQLKGV AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA		
	C5		
	551		600
H41	<u>IGGGTYLGEA</u> GYAIGYSSIS AGGNWIICKGT ASGNSRGHFG ASASVGYQW.		
PMC21	<u>IGGGTYRGEA</u> GYAIGYSSIS DGGNWIICKGT ASGNSRGHFG ASASVGYQW.		
H41Studel	IGGGTYLGEA GYAIGYSSIS AGGNWIICKGT ASGNSRGHFG ASASVGYQW.		
PMC21Bglde1	IGGGTYRGEA GYAIGYSSIS DGGNWIICKGT ASGNSRGHFG ASASVGYQW.		
PMC21C1C5	IGGGTYRGEA GYAIGYSSIS DGGNWIICKGT ASGNSRGHFG ASASVGYQW.		
	C5		

1 50
 H41 MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVQAS
 H41Studel MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 PMC21Bglde1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 C1

51 100
 H41 ATDED...EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE
 PMC21 ANNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
 H41Studel ATDE.....
 PMC21Bglde1 ANNE.....
 PMC21C1C5 AN
 V1

101 150
 H41 FVDPYIVVTL KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK
 PMC21 GVLTAREITL KAGDNLKIKO NGTN..... FTYSLKKDL TDLSVGTEK
 H41Studel
 PMC21Bglde1
 PMC21C1C5
 V1 C2 V2 C3

151 200
 H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
 PMC21 LSFSAHGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
 H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
 PMC21Bglde1 LSFSANGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
 PMC21C1C5
 C3 V3

201 250
 H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT
 PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT
 H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT
 PMC21Bglde1 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT
 PMC21C1C5
 V3 C4 V4 C5

251 300
 H41 YDTVEFLSAD TKTNTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG
 PMC21 YDTVEFLSAD TKTNTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
 H41Studel YDTVEFLSAD TKTNTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG
 PMC21Bglde1 YDTVEFLSAD TKTNTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
 PMC21C1C5 YDTVEFLSAD TKTNTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
 C5

301 350
 H41 KGENGSSTD~~E~~ GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
 PMC21 KGENGSSTD~~E~~ GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
 H41Studel KGENGSSTD~~E~~ GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
 PMC21Bglde1 KGENGSSTD~~E~~ GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
 PMC21C1C5 KGENGSSTD~~E~~ GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
 C5

351 400
 H41 SGTKVTFAS~~G~~ NGTTATVSKD DQGNITVKYD VNVDALNVN QLQNSGWNL
 PMC21 SGTNVTFAS~~G~~ KGTATVSKD DQGNITVMD VNVDALNVN QLQNSGWNL
 H41Studel SGTKVTFAS~~G~~ NGTTATVSKD DQGNITVKYD VNVDALNVN QLQNSGWNL
 PMC21Bglde1 SGTNVTFAS~~G~~ KGTATVSKD DQGNITVMD VNVDALNVN QLQNSGWNL
 PMC21C1C5 SGTNVTFAS~~G~~ KGTATVSKD DQGNITVMD VNVDALNVN QLQNSGWNL
 C5